Table S.1 – *S. pombe* Rab family

Name	Accession
Ypt1	S04590
Ypt2	S12790
Ypt3	S10026
Ypt4	CAB11239
Ypt5	S34729
Ryh1	S12789
Ypt7	O94655

Table S.2 – *S.cerevisiae* Rab family

Name	Accession
Ypt1	NP_116615
Sec4	NP_116650
Ypt31	NP_010948
Ypt32	NP_011305
Ypt51	S43399
Ypt52	NP_012939
Ypt53	NP_014306
Ypt6	NP_013363
Ypt7	NP_013713
Ypt10	NP_009823
Ypt11¶	NP_014095

¶ sequence exhibits large N-terminal extension

Table S.3 – *C. elegans* Rab family

Accession	Proposed name
AAC69218	CeRab1
AAB52431	CeRab2
AAB16980	CeRab3
CAB04205	CeRab5
AAC69020	CeRab6A
CAA77590	CeRab6B
CAA91357	CeRab7
T33855[c]	CeRab8
AAC48200	CeRab10A
AAC48200[c]	CeRab10B
AAB54158	CeRab11A
CAB07678	CeRab11B
CAB01884	CeRab14
CAB60605	CeRab19
AAK29988[¶, c]	CeRab18
CAA91296	CeRab21
CAB54484	CeRab27
CAA21582[CAAX]	CeRab28
CAA21489	CeRab30
CAA84705[¶]	CeRab33
CAB57899	CeRab35
AAB52888	CeRab37
CAA87774[c]	CeRab39
AAK39204[CAAX]	CeRabY1
CAA20282[¶]	CeRabY2
AAC47067[c]	CeRabY3
CAB07357	CeRabY4
CAB07356	CeRabY5
AAA81090[¶,CAAX]	CeRabY6

[c] Sequence does not contain C-terminal cysteines
[CAAX] Sequence contains a single cysteine in the context of a CAAX box
[¶] Sequence exhibits large N- or C- terminal extension

Table S.4 – *D. melanogaster* Rab family

Accession	Proposed name
AAF55873	DmRab1
AAF57381	DmRab2
AAF58762	DmRab3
AAF57831	DmRab4
AAF51265	DmRab5
AAF53168	DmRab6
AAF56218	DmRab7
AAF49101[CAAX]	DmRab8
AAF53798	DmRab9
AAF50924	DmRab10
AAF55850	DmRab11
AAF53390	DmRab14
AAF46057	DmRab18
AAF50452[CAAX]	DmRab19
AAF45341	DmRab21
AAF51970[CAAX]	DmRab23
AAF51708[CAAX,¶]	DmRab26
AAF45634	DmRab27
AAF52477[c]	DmRab30
AAF58970[c]	DmRab32
AAF45371	DmRab35
AAF46271	DmRab39
AAF48164[¶]	DmRab40
AAF47018	DmRabX1/chrowded
AAF46585[c]	DmRabX2
AAF47981[c]	DmRabX3
AAF56345[¶]	DmRabX4
AAF47546[c]	DmRabX5
AAF47406	DmRabX6

[c] Sequence does not contain C-terminal cysteines
[CAAX] Sequence contains a single cysteine in the context of a CAAX box
[¶] Sequence exhibits large N- or C- terminal extension

Table S.5 – *A. thaliana* Rab family

Accession number	Database name	Group	type	isoform	Proposed name
P28185	ARA2	A	1	a	AtRabA1a
Q39222	RAB11	A	1	b	AtRabA1b
BAB09217		A	1	c	AtRabA1c
T04872		A	1	d	AtRabA1d
T04539		A	1	e	AtRabA1e
BAB10106		A	1	f	AtRabA1f
BAA97069		A	1	g	AtRabA1g
F84750		A	1	h	AtRabA1h
AAF16749		A	1	i	AtRabA1i
O04486	RAB11C	A	2	a	AtRabA2a
AAF79570		A	2	b	AtRabA2b
Q96283	RAB11A	A	2	c	AtRabA2c
BAB09761	RAB11	A	2	d	AtRabA2d
AAF97325		A	3	-	AtRabA3
BAB11663		A	4	a	AtRabA4a
T06105	GB3	A	4	b	AtRabA4b
BAB09048		A	4	c	AtRabA4c
BAB01966		A	4	d	AtRabA4d
AAD22360		A	4	e	AtRabA4e
BAB09078		A	5	a	AtRabA5a
AAF02165		A	5	b	AtRabA5b
P28187	ARA4	A	5	c	AtRabA5c
G84723		A	5	d	AtRabA5d
P19892	ARA1	A	5	e	AtRabA5e
AAF24834		A	6	a	AtRabA6a
AAF97836[c, ¶]		A	6	b	AtRabA6b
D71440	RAB2A	B	1	a	AtRabB1a
H85191	RAB2 like	B	1	b	AtRabB1b
S71585	GB2	B	1	c	AtRabB1c
U75603	RAB18	C	1	-	AtRabC1
AAF23245		C	2	a	AtRabC2a
T48379		C	2	b	AtRabC2b
AAD00111	ATFp8	D	1	-	AtRabD1
P28188	ARA5	D	2	a	AtRabD2a
BAA97153		D	2	b	AtRabD2b
CAB78756	RAB1C	D	2	c	AtRabD2c
T45901	RAB8	E	1	a	AtRabE1a
BAB08351	ARA3	E	1	b	AtRabE1b
P28186	ARA5 frag.	E	1	c	AtRabE1c
T48378		E	1	d	AtRabE1d
AAF23246		E	1	e	AtRabE1e
BAB32953[c]	ARA6	F	1	-	AtRabF1
P31582		F	2	a	AtRabF2a
T06157		F	2	b	AtRabF2b

Table S.5 – *A. thaliana* Rab family (continued)

Accession number	Database name	Group	type	isoform	Proposed name
BAB08894[c]	RAB7 Like	G	1		AtRabG1
AAD20423		G	2		AtRabG2
T04019	RAB7 Homolog	G	3	a	AtRabG3a
O04157	RAB7	G	3	b	AtRabG3b
BAB02676		G	3	c	AtRabG3c
AAG21568	RAB7D	G	3	d	AtRabG3d
AAD43167	RAB7	G	3	e	AtRabG3e
BAB01810		G	3	f	AtRabG1f
BAA97311		H	1	a	AtRabH1a
T01588		H	1	b	AtRabH1b
T06095		H	1	c	AtRabH1c
H84610		H	1	d	AtRabH1d
T50814		H	1	e	AtRabH1e

[c] Sequence does not contain C-terminal cysteines
¶ Sequence exhibits large N- or C- terminal extension

Table S.6-*H. sapiens* Rab family

Accession	Proposed Name	Bock *et al.* Name	Bock *et al.* Accession
NP_004152	HsRab1a	1a	=
NP_112243	HsRab1b	1b	IGI_M1_CTG16159_31
NP_002856	HsRab2a	2a	=
IGI_M1_CTG53_358[b, c]	HsRab2b	2b	=
NP_002857	HsRab3a	3a	=
NP_002858	HsRab3b	3b	=
IGI_M1_CTG13513_30[b, c]	HsRab3c	3c	=
NP_004274	HsRab3d	3d	=
NP_004569	HsRab4a	4a	=
NP_057238	HsRab4b	4b	=
Splice variant of 4a(?)	-	4c	IGI_M1_CTG4256_3
NP_004153	HsRab5a	5a	=
NP_002859	HsRab5b	5b	=
NP_004574	HsRab5c	5c	=
NP_002860	HsRab6a	6a	=
NP_057661	HsRab6b	6b	=
CAB66661[c]	HsRab6c	6c	IGI_M1_CTG14521_66
NP_004628	HsRab7	7	=
NP_005361[CAAX]	HsRab8a	8a	=
NP_057614[CAAX]	HsRab8b	8b	=
NP_004242	HsRab9a	9a	=
NP_057454	HsRab9b	9b	IGI_M1_CTG16547_21
Same as 9a	-	9c	GI7705963
NP_057215	HsRab10	10	=
NP_004654	HsRab11a	11a	=
NP_004209	HsRab11b	11b	=
Hs18_11181_25_8_3[i, +]	HsRab12	12	IGI_M1_CTG16793_17
NP_002861[CAAX]	HsRab13	13	=
NP_057406	HsRab14	14	=
AL139022	HsRab15	15	IGI_M1_CTG16579_4
BAB14121	HsRab17	17	IGI_M1_CTG16465_9
AAF61433[CAAX]	HsRab18	18	=
IGI_M1_CTG66_16[b, ¶]	HsRab19	41	=
NP_060287	HsRab20	20	=
NP_055814	HsRab21	21	=
AAF00047	HsRab22a	22a	=
NP_006859	HsRab22b	22c	GI583131
IGI_M1_CTG66_20[b]	HsRab22c	22b	=
NP_057361[c]	HsRab23	23	=
BAB13887[i, c]	HsRab24	-	-
NP_065120[c]	HsRab25	25	=
NP_055168	HsRab26	26	=
NP_004571	HsRab27a	27a	=
NP_004154	HsRab27b	27b	=
NP_004240[c]	HsRab28	28a	=

Table S.6-*H. sapiens* Rab family (continued)

Accession	Proposed Name	Bock *et al.* Name	Bock *et al.* Accession
Splice variant of 28(?)	-	28b	P51157
NP_003920	HsRab29	42	-
NP_055303	HsRab30	30	=
NP_006825	HsRab32	32a	=
NP_004785	HsRab33a	33	=
CAB66838	HsRab33b	-	-
AAK09397*, ¶	HsRab34	34	IGI_M1_CTG15917_25
NP_006852	HsRab35	35	=
NP_004905¶	HsRab36	36	=
IGI_M1_CTG16279_23[b]	HsRab37	37	=
P57729[CAAX]	HsRab38	32b	IGI_M1_CTG15576_6
CAA68227	HsRab39a	39	Q14964
IGI_M1_CTG14748_14[b, c]	HsRab39b	38	=
CAB09136[CAAX, ¶]	HsRab40a	40a	O00407
NP_006813[CAAX, ¶]	HsRab40b	40b	=
O60795[b, i, CAAX, ¶]	HsRab40c	40c	=
IGI_M1_CTG19178_2	HsRab41	43	=

*Annotated in GenBank as Rab39(direct submission).
[b] Accession numbers given in Bock, J.*et al.*. (2001) Nature *409*, 839-841. which we could not find in any database. We used the sequences kindly provided by the authors. Note that our annotation differs from the one made in Bock, J.*et al.*. (2001) Nature *409*, 839-841
[i] Incomplete sequence
[c] Sequence does not contain C-terminal cysteines
[CAAX] Sequence contains a single cysteine in the context of a CAAX box
[¶] Sequence exhibits large N- or C- terminal extension
= identical accession number
[+] accession number in NCBI's MapView